

# PICOEUKARYOTIC PLANKTON COMPOSITION

## REVEALED BY HIGH-THROUGHPUT SEQUENCING: FIRST DATA FOR THE ADRIATIC SEA

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### WITH?

Sequencing: **MiSeq platform**  
 TAReuk454FWD1 and TAReukREV3 to amplify the V4 region (~380bp) of the eukaryotic 18S rDNA (Stoeck *et al.*, 2010).  
 Data analysis: **QIIME 1.9.1.** following Kuczynski *et al.* 2012 pipeline.

### WHY?

To determine **picoeukaryotic diversity** in the southern Adriatic Sea.

### WHERE?

The samples were collected **from coastal to open sea** on total of **8 different depths** at three stations in the **southern Adriatic Sea**, during the late winter **BIOTA cruise** conducted in March 2016 (Fig. 1).

### QIIME PIPELINE

### COLLECTION, FILTRATION, DNA ISOLATION

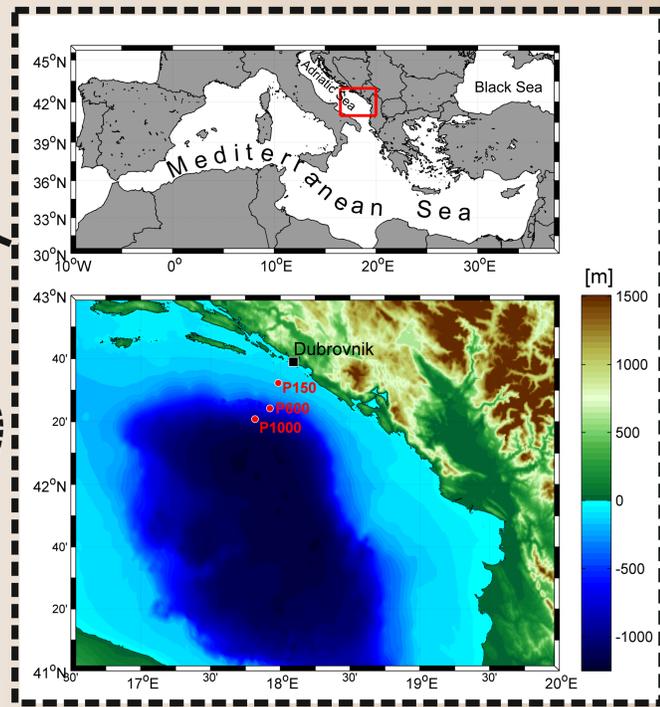
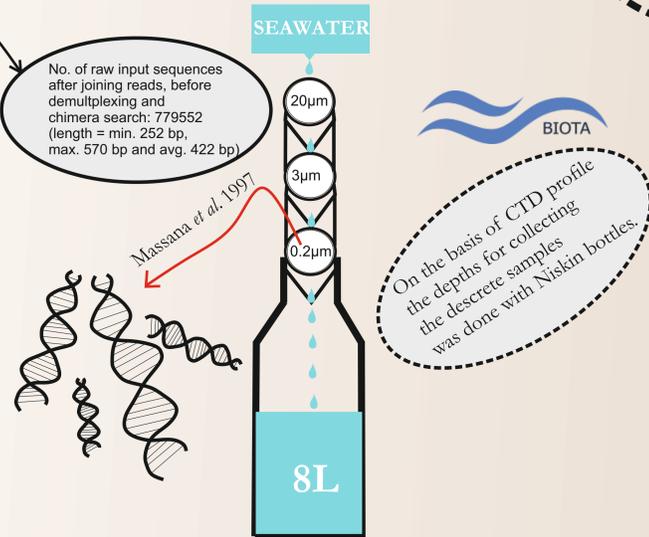
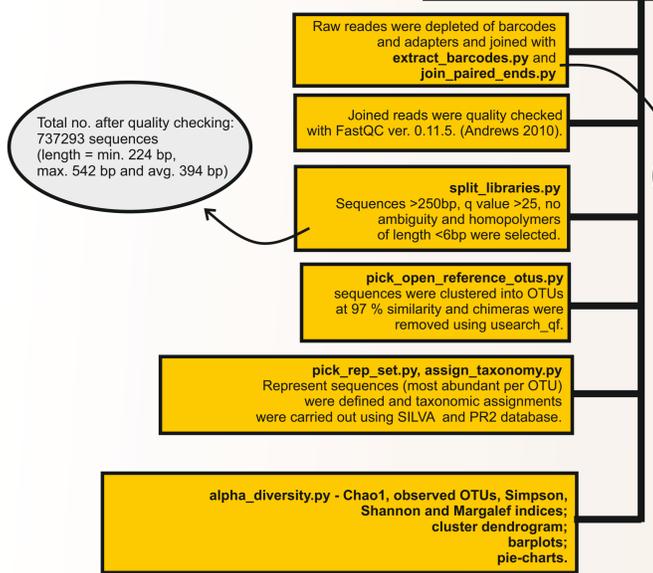


Figure 1. Map of the BIOTA 2016 cruise study area with three stations P150, P600 and P850.

## MAJOR RESULTS

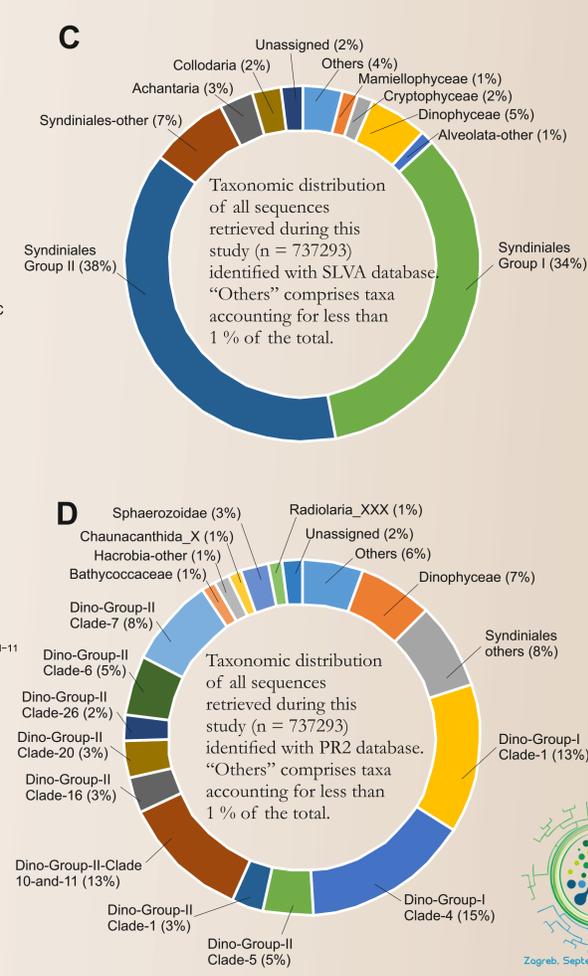
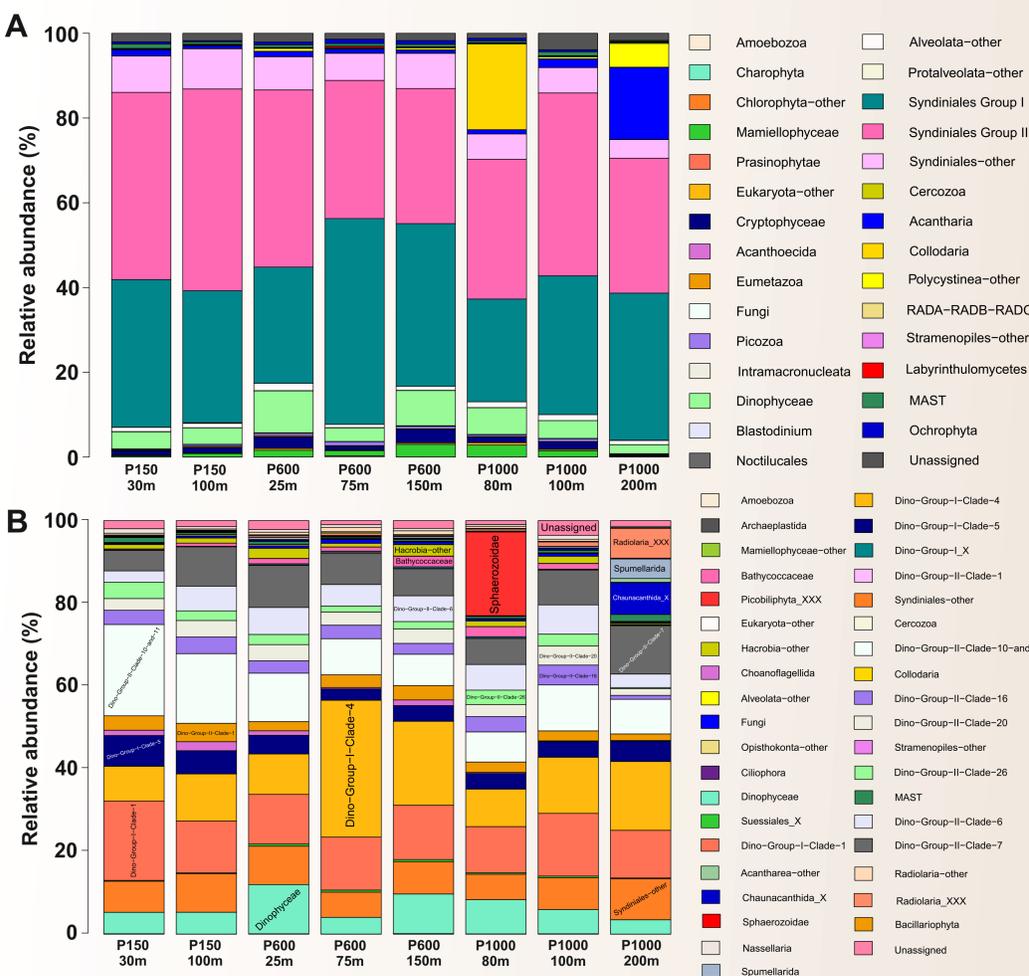
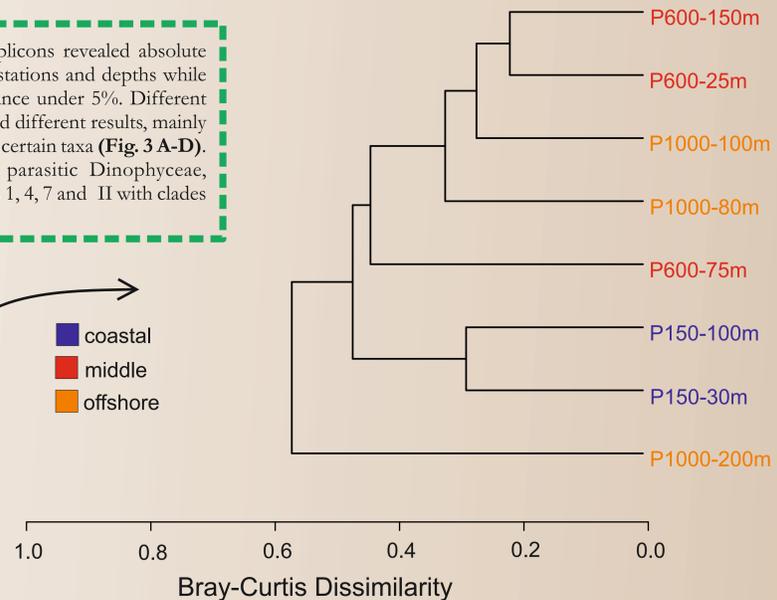
**A**lpha diversity indices (Chao1, Simpson, Shannon and Margalef index) did not differ significantly between samples divided as coastal (blue), middle (red) and offshore (darkorange) (Table 1). Beta-diversity calculated with Bray-Curtis dissimilarity index showed clustering of the coastal, middle and offshore samples with exceptions in samples P600-75m and P1000-200m (Fig. 2) which is in correlation with values of Simpson, Shannon and Chao1 indices for both samples, indicating lower overall species diversity and richness (Table 1).

**H**igh-throughput sequencing of 18S rRNA V4 amplicons revealed absolute dominance of heterotrophic picoeukaryotes at all stations and depths while photosynthetic picoeukaryotes had relative abundance under 5%. Different databases for taxonomical affiliation of clustered OTUs generated different results, mainly in level of taxonomical identification and in relative abundance of certain taxa (Fig. 3 A-D). Heterotrophic picoeukaryotes were mostly represented by parasitic Dinophyceae, Syndiniales group, with dominance of Dino-Groups I with clades 1, 4, 7 and II with clades 10, 11 and 7 (Fig. 3 C-D).

Table 1. Number of sequences, observed OTUs and alpha diversity indices for 8 samples collected in the South Adriatic Sea during BIOTA cruise in March 2016.

Sample	No. of sequences	Observed OTUs	Simpson	Shannon	Margalef	Chao1
P150-30m	81712	1184	0,97	6,88	105,04	1366,01
P150-100m	82376	1197	0,97	6,93	106,03	1354,86
P600-25m	85645	1225	0,97	6,99	108,17	1402,13
P600-75m	71798	1016	0,88	5,65	91,01	1235,38
P600-150m	86890	1126	0,95	6,51	99,21	1394,32
P1000-80m	129774	1243	0,94	6,18	105,77	1432,93
P1000-100m	113550	1241	0,96	6,70	106,84	1371,11
P1000-200m	85548	1056	0,95	6,31	93,17	1231,90

Figure 2. Beta-diversity analysis of 8 Adriatic samples collected at three stations (P150, P600 and P1000) during BIOTA cruise in March 2016. Dendrogram presents the Bray-Curtis dissimilarity between the composition of 8 picoeukaryotic communities from coastal (blue), middle (red) and offshore (darkorange) water samples.



**P**hotosynthetic picoeukaryotes were represented with class Mamiellophyceae, family Bathycoccaceae which had higher relative abundance in middle and open waters. Interesting shifting pattern in picoeukaryotic community was observed at open sea station P1000, depth 80 m where radiolarians from order Collocladia, family Sphaerozoidea appeared in high relative abundance (23%) which was particularly interesting with regard to ongoing climate changes and impact on the Adriatic Sea (Fig. 3B). According to Biard *et al.* 2017, family Sphaerozoidea is more abundant than Collosphaeridae in west Mediterranean, closer to the Atlantic, and Collosphaeridae should prevail moving to east Mediterranean (one exception was station in the South Adriatic Sea, where Biard *et al.* 2017, documented both families in equal ratio).

### ACKNOWLEDGMENTS

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